

FIGURE 1

cDNA sequence of wild type amFP486

ATGGCTCTTTCAAACAAGTTTATCGGAGATGACATGAAAATGACCTACCATATGGATG
GCTGTGTCAATGGGCATTACTTTACCGTCAAAGGTGAAGGCAACGGGAAGCCATACGA
AGGGACGCAGACCTCGACTTTTAAAGTCACCATGGCCAACGGTGGGCCCCCTTGCATT
TCCTTTGACATACTATCTACAGTGTTCAAGTATGGAAATCGATGCTTTACTGCGTATC
CTACCAGTATGCCCGACTATTTCAAACAAGCATTTCTGACGGAATGTCATATGAAAG
GACTTTTACCTATGAAGATGGAGGAGTTGCTACAGCCAGTTGGGAAATAAGCCTTAAA
GGCAACTGCTTTGAGCACAAATCCACGTTTTCATGGAGTGAACCTTCTGCTGATGGAC
CTGTGATGGCGAAGATGACAACCTGGTTGGGACCCATCTTTTGAGAAAATGACTGTCTG
CGATGGAATATTGAAGGGTGATGTCACCGCGTTCCTCATGCTGCAAGGAGGTGGCAAT
TACAGATGCCAATTCCACACTTCTTACAAGACAAAAAACCAGGTGACGATGCCACCAA
ACCATGCGGTGGAACATCGCATTGCGAGGACCGACCTTGACAAAGGTGGCAACAGTGT
TCAGCTGACGGAGCACGCTGTTGCACATATAACCTCTGTTGTCCCTTTC (SEQ ID
NO:01)

amino acid sequence of wild type amFP486

MALSNKFIGD DMKMTYHMDG CVNGHYFTVK GEGNGKPYEG TQTSTFKVTM ANGGPLAFSF
DILSTVFKYG NRCFTAYPTS MPDYFKQAFP DGMSYERTFT YEDGGVATAS WEISLKGNCF
EHKSTFHGVN FPAAGPVMAM MTTGWDPSE KMTVCDGILK GDVTAFLMLQ GGGNYRCQFH
TSYKTKKPVT MPPNHAVEHR IARTDLKGG NSVQLTEHAV AHITSVVPF
(SEQ ID NO:02)

10005922.120401

Figure 2

cDNA sequence of wild type cFP484

TATAGGANCATNNGGGNGATTGGGGTCCAAAGCATTGTAACCAACGCAGATAACCCCCAG
 TGGTNTCAAACGCAGANAACGCGGGAACATTGGAAAATTGANTNTTAAGGAGGCAAGGAA
 TCGGGAGTAAAGTTGCGAGAAACTGAAAAATGAAAGTGTAATTTGTGTTCTGCCTGTCC
 TTCTTGGTCCTCGCCATCACAAACGCGAACATTTTTTTGAGAAACGAGGCTGACTTAGAA
 GAGAAGACATTGAGAATACCAAAGCTCTAACCACCATGGGTGTGATTAAACCAGACATG
 AAGATTAAGCTGAAGATGGAAGGAAATGTAAACGGGCATGCTTTTGTGATCGAAGGAGAA
 GGAGAAGGAAAGCCTTACGATGGGACACACACTTTAAACCTGGAAGTGAAGGAAGGTGCG
 CCTCTGCCTTTTTCTTACGATATCTTGTCAAACGCGTTCAGTACGGAACAGAGCATTG
 ACAAATACCCAGACGATATAGCAGACTATTTCAAGCAGTCGTTTCCCGAGGGATATTCC
 TGGGAAAGAACCATGACTTTTGAAGACAAAGGCATTGTCAAAGTGAAAAGTGACATAAGC
 ATGGAGGAAGACTCCTTTATCTATGAAATTCGTTTTGATGGGATGAACTTTCCTCCCAAT
 GGTCCGGTTATGCAGAAAAAACTTTGAAGTGGGAACCATCCACTGAGATTATGTACGTG
 CGTGATGGAGTGCTGGTCCGAGATATTAGCCATTCTCTGTTGCTGGAGGGAGGTGGCCAT
 TACCGATGTGACTTCAAAGTATTTACAAAGCAAAAAAGTTGTCAAATTGCCAGACTAT
 CACTTTGTGGACCATCGCATTGAGATCTTGAACCATGACAAGGATTACAACAAAGTAACG
 CTGTATGAGAATGCAGTTGCTCGCTATTCTTTGCTGCCAAGTCAGGCCTAGACAACAAGG
 ATACTGAAAACATATTTGTCTGAGGGTTTGTGTTGTTTTTAAAGACATCAGCTCAGCA
 TTCGTTAGTTGTAACAAAAATAGCTTTAATTTTTTGGTGGGATTAAATCATAGGGATTG
 TTTTAGTAATCATTTTGCTTAATAAAAAAGTGCCTTG (SEQ ID NO:03)

amino acid sequence of wild type cFP484

M K C K F V F C L S
 F L V L A I T N A N I F L R N E A D L E
 E K T L R I P K A L T T M G V I K P D M
 K I K L K M E G N V N G H A F V I E G E
 G E G K P Y D G T H T L N L E V K E G A
 P L P F S Y D I L S N A F Q Y G N R A L
 T K Y P D D I A D Y F K Q S F P E G Y S
 W E R T M T F E D K G I V K V K S D I S
 M E E D S F I Y E I R F D G M N F P P N
 G P V M Q K K T L K W E P S T E I M Y V
 R D G V L V G D I S H S L L L E G G G H
 Y R C D F K S I Y K A K K V V K L P D Y
 H F V D H R I E I L N H D K D Y N K V T
 L Y E N A V A R Y S L L P S Q A (SEQ ID NO:04)

10006922-120401

Figure 3

cDNA sequence of zFP506

ATGGCTCAGTCAAAGCACGGTCTAACAAAAGAAATGACAATGAAATACCGTATGGAAGGGTGC
GTCGATGGACATAAATTTGTGATCACGGGAGAGGGCATTGGATATCCGTTCAAAGGGAAACAG
GCTATTAATCTGTGTGTGGTCGAAGGTGGACCATTGCCATTTGCCGAAGACATATTGTCAGCT
GCCTTTATGTACGGAAACAGGGTTTTCTACTGAATATCCTCAAGACATAGCTGACTATTTCAAG
AACTCGTGTCTGCTGGTTATACATGGGACAGGTCTTTCTCTTTGAGGATGGAGCAGTTTGC
ATATGTAATGCAGATATAACAGTGAGTGTTGAAGAAAAGTGCATGTATCATGAGTCCAAATTT
TATGGAGTGAATTTTCCTGCTGATGGACCTGTGATGAAAAAGATGACAGATAACTGGGAGCCA
TCCTGCGAGAAGATCATACCAGTACCTAAGCAGGGGATATTGAAAGGGGGATGTCTCCATGTAC
CTCCTTCTGAAGGATGGTGGGCGTTTACGGTGCCAATTCGACACAGTTTACAAAGCAAAGTCT
GTGCCAAGAAAGATGCCGGAAGTGGCACTTCATCCAGCATAAGCTCACCCGTGAAGACCGCAGC
GATGCTAAGAATCAGAAATGGCATCTGACAGAACATGCTATTGCATCCGGATCTGCATTGCCC
(SEQ ID NO:05)

amino acid sequence of zFP506

MAQSKHGLTK EMTMKYRMEG CVDGHKFEVIT GEGIGYPFKG KQAINLCVVE GGPLPFAEDI LSAAFNYGNR VFTEYPQDIA
DYFKNSCPAG YTWDRSFLFE DGAVCICNAD ITVSVEENCM YHESKFGVN FPDGPMKK MTDNWEPSCE KIIPVKQGI
LKGDVSMYLL LKDGRLRCQ FDTVYKAKSV PRKMPDWHFI QHKLTREDRS DAKNQKWHLT EHAIASGSAL P
(SEQ ID NO:06)

10006522-120401

Figure 4

cDNA sequence of zFP538

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gagttgagtt tctcgacttc agttgtatca attttggggc atcaagcgat ctattttcaa
catggctcat tcaaagcacg gtctaaaaga agaaatgaca atgaaatacc acatggaagg
gtgCGTcaac ggacataaat ttgtgatcac gggcgaaggc attggatatc cgttcaaagg
gaaacagact attaatctgt gtgtgatcga agggggacca ttgccathtt ccgaagacat
attgtcagct ggctttaagt acggagacag gattttcact gaatatcctc aagacatagt
agactatttc aagaactcgt gtctgtctgg atatacatgg ggcagggtctt ttctctttga
ggatggagca gtctgcatat gcaatgtaga tataacagtg agtgtcaaag aaaactgcat
ttatcataag agcatattta atggaatgaa ttttcctgct gatggacctg tgatgaaaaa
gatgacaact aactgggaag catcctgcga gaagatcatg ccagtaccta agcaggggat
actgaaaggg gatgtctcca tgtacctcct tctgaaggat ggtgggcgtt accggtgccca
gttcgacaca gtttaciaag caaagtctgt gccaaagtaag atgccggagt ggcacttcat
ccagcataag ctctccgtg aagaccgcag cgatgctaag aatcagaagt ggcagctgac
agagcatgct attgcattcc cttctgcctt ggctgataa gaatgtagtt ccaacatttt
aatgcatgtg cttgtcaatt attctgataa aaatgtagtt gagttgaaaa cagacaagta
caaataaagc acatgtaaat cgtct      (SEQ ID NO:07)

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amino acid sequence of zFP538

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Met Ala His Ser Lys His Gly Leu Lys Glu Glu Met Thr Met Lys
Tyr His Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr
Gly Glu Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn
Leu Cys Val Ile Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile
Leu Ser Ala Gly Phe Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr
Pro Gln Asp Ile Val Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly
Tyr Thr Trp Gly Ser Phe Leu Phe Glu Asp Gly Ala Val Cys Ile
Cys Asn Val Asp Ile Thr Val Ser Val Lys Glu Asn Cys Ile Tyr
His Lys Ser Ile Phe Asn Gly Met Asn Phe Pro Ala Asp Gly Pro
Val Met Lys Lys Met Thr Thr Asn Trp Glu Ala Ser Cys Glu Lys
Ile Met Pro Val Pro Lys Gln Gly Ile Leu Lys Gly Asp Val Ser
Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr Arg Cys Gln Phe
Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser Lys Met Pro Glu
Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp Arg Ser Asp
Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile Ala Phe
Pro Ser Ala Leu Ala (SEQ ID NO:08)

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100069221.120401

FIGURE 5

cDNA sequence of dsFP483

ACGGTCAGGGACACGGTGACCCACTTTGGTATTCTAACAAAATGAGTTGGTCCAAGAGTG
 TGATCAAGGAAGAAATGTTGATCGATCTTCATCTGGAAGGAACGTTCAATGGGCACTACT
 TTGAAATAAAAGGCAAAGGAAAAGGGAAGCCTAATGAAGGCACCAATACCGTCACGCTCG
 AGGTTACCAAGGGTGGACCTCTGCCATTTGGTTGGCATATTTTGTGCCCCACAATTTTCAGT
 ATGGAAACAAGGCATTTGTCCACCACCCTGACGACATACCTGATTATCTAAAGCTGTCAT
 TTCCGGAGGGATATACATGGGAACGGTCCATGCACTTTGAAGACGGTGGCTTGTGTTGTA
 TCACCAATGATATCAGTTTGACAGGCAACTGTTTCAACTACGACATCAAGTTCACTGGCT
 TGAACCTTTCCTCCAAATGGACCCGTTGTGCAGAAGAAGACAACCTGGCTGGGAACCGAGCA
 CTGAGCGTTTGTATCCTCGTGATGGCGTGTGTAGTAGGAGACATCCATCATGCTCTCACAG
 TGGAAGGAGGTGGTCATTACGTATGTGACATTAAAACTGTTTACAGGGCCAAGAAGCCCG
 TAAAGATGCCAGGGTATCACTATGTTGACACCAAACCTGGTTATAAGGAGCAACGACAAAG
 AATTCATGAAAGTTGAGGAGCATGAAATCGCCGTTGCACGCCACCATCCGCTCCAAAGCC
 AATGAAGCTTAAGTAAAGCAAAAAGGTGACGAGGCATGATAGTATGACATGATAGTATGA
 CATGATAGTATGACATGATAGTAAGAATTGTAAGCAAAAGGCTTTGCTTATTAACTTGT
 AATTGAAAAC (SEQ ID NO:09)

amino acid sequence of dsFP483

M S W S K S V
 I K E E M L I D L H L E G T F N G H Y F
 E I K G K G K G K P N E G T N T V T L E
 V T K G G P L P F G W H I L C P Q F Q Y
 G N K A F V H H P D D I P D Y L K L S F
 P E G Y T W E R S M H F E D G G L C C I
 T N D I S L T G N C F N Y D I K F T G L
 N F P P N G P V V Q K K T T G W E P S T
 E R L Y P R D G V L I G D I H H A L T V
 E G G G H Y V C D I K T V Y R A K K P V
 K M P G Y H Y V D T K L V I R S N D K E
 F M K V E E H E I A V A R H H P L Q S Q
 (SEQ ID NO:10)

F0702T"2269000T

FIGURE 6

cDNA sequence of drFP583

ATGAGGTCTTCCAAGAATGTTATCAAGGAGTTCATGAGGTTTAAAGGTTTCGCATGGAAGGAACGGTCAATGGGCACGAGT
 TTGAAATAGAAGGCGAAGGAGAGGGGAGGCCATACGAAGGCCACAATACCGTAAAGCTTAAGGTAACCAAGGGGGGACC
 TTTGCCATTTGCTTGGGATATTTTGTCAACCAATTTTCAAGTATGGAAGCAAGGTATATGTCAAGCACCTGCCGACATA
 CCAGACTATAAAAAAGCTGTCAATTCCTGAAGGATTTAAATGGGAAAGGGTCATGAACCTTTGAAGACGGTGGCGTCGTTA
 CTGTAACCCAGGATTCCAGTTTGCAGGATGGCTGTTTCATCTACAAGGTCAAGTTCATTGGCGTGAACCTTCCTTCCGA
 TGGACCTGTTATGCAAAAGAAGACAATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTGATGGCGTGTGAAA
 GGAGAGATTATAAGGCTCTGAAGCTGAAAGACGGTGGTCATTACCTAGTTGAATTCAAAAGTATTTACATGGCAAAGA
 AGCCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCAACTGGATATAACAAGCCACAACGAAGACTATACAATCGT
 TGAGCAGTATGAAAGAACCAGGGGACGCCACCATCTGTTCCCTTTAA (SEQ ID NO:11)

cDNA sequence of drFP583.1

GTCTCTCCCAAGCAGTGGTATCAACGCAGAGTACGGGGGAGTTTCAGCCAGTGACGGT
 CAGTGACAGGGTGAGCCACTTGGTATACCAACAAAAATGAGGTCTTCCAAGAATGTTA
 TCAAGGAGTTTCATGAGGTTTAAAGGTTTCGCATGGAAGGAACGGTCAATGGGCACGAGT
 TTGAAATAGAAGGCGAAGGAGAGGGGAGGCCATACGAAGGCCACAATACCGTAAAGC
 TTAAGGTAACCAAGGGGGGACCCTTTGCCATTTGCTTGGGATATTTTGTCAACCAAT
 TTCAGTATGGAAGCAAGGTATATGTCAAGCACCTGCCGACATACCAGACTATAAAA
 AGCTGTCAATTCCTGAAGGATTTAAATGGGAAAGGGTCATGAACCTTTGAAGACGGTG
 GCGTCGTTACTGTAACCCAGGATTCCAGTTTGCAGGATGGCTGTTTCATCTACAAGT
 CAAGTTCATTGGCGTTGAACCTTTCCTCCGATGGACCTGTTATGCAAAAGAAGACAA
 TGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTGATGGCGTGTGAAAGGAG
 AGATTACATAAGGCTCTGAAGCTGAAAGACGGTGGTCATTACCTAGTTGAATTCAAAA
 GTATTTACATGGCAAAGAAGCCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCA
 AACTGGATATAACAAGCCACAACGAAGACTATACAATCGTTGAGCAGTATGAAAGAA
 CCGAGGGGACGCCACCATCTGTTCCCTTTAAGGCTGAACCTTGGCTCAGACGTGGGTGAG
 CGGTAATGACCACAAAAGGCAGCGAAGAAAAACCATGATCGTTTTTTTTAGGTTGGC
 AGCCTGAAATCGTAGGAAATACATCAGAAATGTTACAAACAGG (SEQ ID NO:45)

amino acid sequence of drFP583

MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILSPQFQ
 YGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIGVNFPSD
 GPVMQKKTMGWEASTERLYPRDGVLLKGEIHKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYVDSK
 LDITSHNEDYTIVEQYERTEGRHHLFL (SEQ ID NO:012)

amino acid sequence of drFP583.1

Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys
 Val Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu
 Gly Glu Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys
 Leu Lys Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile
 Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His
 Pro Ala Asp Ile Pro Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly
 Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly Gly Val Val
 Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Cys Phe Ile Tyr
 Lys Ser Ser Ser Leu Ala Leu Asn Phe Pro Ser Asp Gly Pro Val
 Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Leu
 Gly His Tyr Leu Val Glu Phe Lys Ser Ile Ile Met Ala Lys Lys
 Pro Val Gln Leu Pro Gly Tyr Tyr Tyr Val Asp Ser Lys Leu Asp
 Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu
 Arg Ser Glu Gly Arg His His Leu Phe Leu
 (SEQ ID NO:46)

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FIGURE 7

Amino Acid and Nucleotide Sequence for asFP600

ATGGCTTCCTTTTTTAAAGAAGACTATGCCCTTTAAGACGACCATTGAAGGGACGGTTAATGGCCAC
TACTTCAAGTGTACAGGAAAAGGAGAGGGCAACCCATTTGAGGGTACGCAGGAAATGAAGATAGAG
GTCATCGAAGGAGGTCCATTGCCATTTGCCCTTCCACATTTTGTCAACGAGTTGTATGTACGGTAGT
AAGGCCTTCATCAAGTATGTGTTCAGGAATTCCTGACTACTTCAAGCAGTCTTTCCTGAAGGTTTT
ACTTGGGAAAGAACCACAACCTACGAGGATGGAGGCTTTCTTACAGCTCATCAGGACACAAGCCTA
GATGGAGATTGCCTCGTTTACAAGGTCAAGATTCTTGGTAATAATTTTCCTGCTGATGGCCCCGTG
ATGCAGAACAAAGCAGGAAGATGGGAGCCATCCACCGAGATAGTTTATGAAGTTGACGGTGTCTTG
CGTGGACAGTCTTTGATGGCCCTTAAGTGCCCTGGTGGTTCGTCATCTGACTTGCCATCTCCATACT
ACTTACAGGTCCAAAAAACCAGCTGCTGCCCTGAAGATGCCAGGATTTTCATTTTGAAGATCATCGC
ATCGAGATAATGGAGGAAGTTGAGAAAGGCAAGTGCTATAAACAGTACGAAGCAGCAGTGGGCAGG
TACTGTGATGCTGCTCCATCCAAGCTTGGACATAAC (SEQ ID NO:13)

Amino acid

MASFLKKTMP FKTTIEGTVN GHYFKCTGKG EGNPFEGTQE MKIEVIEGGP LPFAFHILST
SCMYGSKTFI KYVSGIPDYF KQSFPEGFTW ERTTTYEDGG FLTAHQDTSI DGDCLVYKVK
ILGNNFPADG PVMQNKAGRW EPATEIVYEV DGVLRGQSLM ALKCPGGRHL TCHLHTTYRS
KKPAAALKMP GFHFDHRIE IMEEVEKGKC YKQYEAAGR YCDAAPSKLG HN (SEQ ID
NO:14)

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Figure 8

cDNA sequence of dgFP512

attcacctcg gtgatttgta agagaaagga tcaccatcaa gagaagagct gtaaaagtta 60
 atattttact gtactttctac cagcatgagt gcacttaaag aagaaatgaa aatcaacctt 120
 acaatggaag gtgttggttaa cgggcttcca ttttaagatcc gtgggggatgg aaaaggcaaa 180
 ccataccagg gatcacagga gttaaccttg acggtggtta aaggcggggc tctgcctttc 240
 tcttatgata ttctgacaac gatgtttcag tacggcaaca gggcattcgt aaactacca 300
 gaggacatac cagatatttt caagcagacc tgttctggtc ctaatggtgg atattcctgg 360
 caaaggacca tgacttatga agacggaggc gtttgactg ctacaagcaa catcagcgtg 420
 gttggcgaca ctttcaatta tgacattcac tttatgggag cgaattttcc tcttgatggt 480
 ccagtgatgc agaaaagaac aatgaaatgg gaaccatcca ctgagataat gtttgaacgt 540
 gatggaatgc tgaggggtga cattgccatg tctctgttgc tgaagggagg gggccattac 600
 cgatgtgatt ttgaaactat ttataaacc aataagggtg tcaagatgcc agattacat 660
 tttgtggacc actgcattga gataacgagt caacaggatt attacaacgt gggtgagctg 720
 accgaggttg ctgaagcccg ctactcttcg ctggagaaaa tcggcaaadc aaaggcgtaa 780
 atccaagcaa tctaagaaaa caacaaggca ttaaaccgaa tcaccgtttt gaatttttcg 840
 ttcggaattt cttggtaaaa ctaggttttag aacgtttcat ttcgctggac ttctttgact 900
 cagctgtaga caagaaaga (SEQ ID NO:15) 919

amino acid sequence of dgFP512

Met Ser Ala Leu Lys Glu Glu Met Lys Ile Asn Leu Thr Met Glu
 Gly Val Val Asn Gly Leu Pro Phe Lys Ile Arg Gly Asp Gly Lys
 Gly Lys Pro Tyr Gln Gly Ser Gln Glu Leu Thr Leu Thr Val Val
 Lys Gly Gly Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Thr Met
 Phe Gln Tyr Gly Asn Arg Ala Phe Val Asn Tyr Pro Glu Asp Ile
 Pro Asp Ile Phe Lys Gln Thr Cys Ser Gly Pro Asn Gly Gly Tyr
 Ser Trp Gln Arg Thr Met Thr Tyr Glu Asp Gly Gly Val Cys Thr
 Ala Thr Ser Asn Ile Ser Val Val Gly Asp Thr Phe Asn Tyr Asp
 Ile His Phe Met Gly Ala Asn Phe Pro Leu Asp Gly Pro Val Met
 Gln Lys Arg Thr Met Lys Trp Glu Pro Ser Thr Glu Ile Met Phe
 Glu Arg Asp Gly Met Leu Arg Gly Asp Ile Ala Met Ser Leu Leu
 Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Glu Thr Ile Tyr
 Lys Pro Asn Lys Val Val Lys Met Pro Asp Tyr His Phe Val Asp
 His Cys Ile Glu Ile Thr Ser Gln Gln Asp Tyr Tyr Asn Val Val
 Glu Leu Thr Glu Val Ala Glu Ala Arg Tyr Ser Ser Leu Glu Lys
 Ile Gly Lys Ser Lys Ala
 (SEQ ID NO:16)

T0402T-2269001

FIGURE 9

cDNA sequence of dmFP592

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agtttcagcc agtgacaggg tgagctgcca ggtattctaa caagatgagt tgttccaaga 60
atgtgatcaa ggagttcatg aggttcaagg ttcgtatgga aggaacggtc aatgggcacg 120
agtttgaaat aaaaggcgaa ggtgaagggg ggccttacga aggtcactgt tccgtaaagc 180
ttatggtaac caagggtgga cctttgccat ttgcttttga tttttgtca ccacaatttc 240
agtatggaag caaggtatat gtcaaacacc ctgccgacat accagactat aaaaagctgt 300
catttcctga gggattttaa tgggaaaggg tcatgaactt tgaagacggg gccgtgggta 360
ctgtatccca agattccagt ttgaaagacg gctgtttcat ctacgaggtc aagttcattg 420
gggtgaactt tccttctgat ggacctgtta tgcagaggag gacacggggc tgggaagcca 480
gctctgagcg tttgtatcct cgtgatgggg tgctgaaagg agacatccat atggctctga 540
ggctggaagg aggcggccat tacctcgttg aattcaaaag tatttacatg gtaaagaagc 600
cttcagtgca gttgccaggc tactattatg ttgactccaa actggatatg acgagccaca 660
acgaagatta cacagtcggt gagcagtatg aaaaaaccca gggacgccac catccgttca 720
ttaagcctct gcagtgaact cggctcagtc atggattagc ggtaatggcc acaaaaggca 780
cgatgatcgt tttttaggaa tgcagccaaa aattgaagggt tatgacagta gaaatacaag 840
caacaggctt tgcttattaa acatgtaatt gaaaac 876

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(SEQ ID NO:17)

amino acid sequence of dmFP592

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Met Ser Cys Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys
Val Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Lys
Gly Glu Gly Glu Gly Arg Pro Tyr Glu Gly His Cys Ser Val Lys
Leu Met Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile
Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His
Pro Ala Asp Ile Pro Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly
Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly Gly Val Val
Thr Val Ser Gln Asp Ser Ser Leu Lys Asp Gly Cys Phe Ile Tyr
Glu Val Lys Phe Ile Gly Val Asn Phe Pro Ser Asp Gly Pro Val
Met Gln Arg Arg Thr Arg Gly Trp Glu Ala Ser Ser Glu Arg Leu
Tyr Pro Arg Asp Gly Val Leu Lys Gly Asp Ile His Met Ala Leu
Arg Leu Glu Gly Gly Gly His Tyr Leu Val Glu Phe Lys Ser Ile
Tyr Met Val Lys Lys Pro Ser Val Gln Leu Pro Gly Tyr Tyr Tyr
Val Asp Ser Lys Leu Asp Met Thr Ser His Asn Glu Asp Tyr Thr
Val Val Glu Gln Tyr Glu Lys Thr Gln Gly Arg His His Pro Phe
Ile Lys Pro Leu Gln

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(SEQ ID NO:18)

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Figure 10

	M	A	L	S	N	E	F	I	G	D	D	M	K	M
676	ATG	GCC	CTG	TCC	AAC	GAG	TTC	ATC	GGC	GAC	GAC	ATG	AAG	ATG
	TAC	CGG	GAC	AGG	TTG	TTC	AAG	TAG	CCG	CTG	CTG	TAC	TTC	TAC
	T	Y	H	M	D	G	C	V	N	G	H	Y	F	T
721	ACC	TAC	CAC	ATG	GAC	GGC	TGC	AAC	GGC	CAC	TAC	TTC	ACC	GTG
	TGG	ATG	GTG	TAC	CTG	CCG	ACG	CAC	TTG	CCG	GTG	ATG	AAG	TGG
	K	G	E	G	S	G	K	P	Y	E	G	T	Q	T
766	AAG	GGC	GAG	GGC	AGC	GGC	AAG	CCC	TAC	GAG	GGC	ACC	CAG	ACC
	TTC	CCG	CTC	CCG	TCG	CCG	TTC	GGG	ATG	CTC	CCG	TGG	GTC	TGG
	T	F	K	V	T	M	A	N	G	G	P	L	A	F
811	ACC	TTC	AAG	GTG	ACC	ATG	GCC	AAC	GGC	GGC	CCC	CTG	GCC	TTC
	TGG	AAG	TTC	CAC	TGG	TAC	CCG	TTG	CCG	CCG	GGG	GAC	CCG	AAG
	F	D	I	L	S	T	V	F	M	Y	G	N	R	C
856	TTC	GAC	ATC	CTG	TCC	ACC	GTG	TTC	ATG	TAC	GGC	AAC	CGC	TGC
	AAG	CTG	TAG	GAC	AGG	TGG	CAC	AAG	TAC	ATG	CCG	TTG	GCG	ACG
	T	A	Y	P	T	S	M	P	D	Y	F	K	Q	A
901	ACC	GCC	TAC	CCC	ACC	AGC	ATG	CCC	GAC	TAC	TTC	AAG	CAG	GCC
	TGG	CCG	ATG	GGG	TGG	TCG	TAC	GGG	CTG	ATG	AAG	TTC	GTC	CCG
	P	D	G	M	S	Y	E	R	T	F	T	Y	E	D
946	CCC	GAC	GGC	ATG	TCC	TAC	GAG	AGA	ACC	TTC	ACC	TAC	GAG	GAC
	GGG	CTG	CCG	TAC	AGG	ATG	CTC	TCT	TGG	AAG	TGG	ATG	CTC	CTG
	G	V	A	T	A	S	W	E	I	S	L	K	G	N
991	GGC	GTG	GCC	ACC	GCC	AGC	TGG	GAG	ATC	AGC	CTG	AAG	GGC	AAC
	CCG	CAC	CGG	TGG	CGG	TCG	ACC	CTC	TAG	TCG	GAC	TTC	CCG	TTG
	F	E	H	K	S	T	F	H	G	V	N	F	P	A
1036	TTC	GAG	CAC	AAG	TCC	ACC	TTC	CAC	GGC	GTG	AAC	TTC	CCC	GCC
	AAG	CTC	GTG	TTC	AGG	TGG	AAG	GTG	CCG	CAC	TTG	AAG	GGG	CGG
	G	P	V	M	A	K	K	T	T	G	W	D	P	S
1081	GGC	CCC	GTG	ATG	GCC	AAG	AAG	ACC	ACC	GGC	TGG	GAC	CCC	TCC
	CCG	GGG	CAC	TAC	CGG	TTC	TTC	TGG	TGG	CCG	ACC	CTG	GGG	AGG
	E	K	M	T	V	C	D	G	I	L	K	G	D	V
1126	GAG	AAG	ATG	ACC	GTG	TGC	GAC	GGC	ATC	TTG	AAG	GGC	GAC	GTG
	CTC	TTC	TAC	TGG	CAC	ACG	CTG	CCG	TAG	AAC	TTC	CCG	CTG	CAC
	A	F	L	M	L	Q	G	G	G	N	Y	R	C	Q
1171	GCC	TTC	CTG	ATG	CTG	CAG	GGC	GGC	AAC	TAC	AGA	TGC	CAG	TTC
	CGG	AAG	GAC	TAC	GAC	GTC	CCG	CCG	CCG	TTG	ATG	TCT	ACG	GTC
	H	T	S	Y	K	T	K	K	P	V	T	M	P	P
1216	CAC	ACC	TCC	TAC	AAG	ACC	AAG	AAG	CCC	GTG	ACC	ATG	CCC	CCC
	GTG	TGG	AGG	ATG	TTC	TGG	TTC	TTC	GGG	CAC	TGG	TAC	GGG	GGG
	H	V	V	E	H	R	I	A	R	T	D	L	D	K
1261	CAC	GTG	GTG	GAG	CAC	CGC	ATC	GCC	AGA	ACC	GAC	CTG	GAC	AAG
	GTG	CAC	CAC	CTC	GTG	GCG	TAG	CGG	TCT	TGG	CTG	GAC	CTG	TTC
	G	N	S	V	Q	L	T	E	H	A	V	A	H	I
1306	GGC	AAC	AGC	GTG	CAG	CTG	ACC	GAG	CAC	GCC	GTG	GCC	CAC	ATC
	CCG	TTG	TCG	CAC	GTC	GAC	TGG	CTC	GTG	CGG	CAC	CGG	GTG	TAG
	S	V	V	P	F	*								
1351	TCC	GTG	GTG	CCC	TTC	TGA								
	AGG	CAC	CAC	GGG	AAG	ACT								

(SEQ ID NO:27 & 28)

10006922-120401

Figure 11

Non-aggregating mutant FP3-NA was generated from zFP506-N65M (non-humanized version). In comparison with zFP506-N65M, FP3-NA contains two additional amino acid substitutions - K5E and K10E. Also, one accidental nucleotide substitution was introduced due to PCR mistake (double underline).

Cloning into pQE30 was done using BamHI and HindIII sites:

GGA TCC GCT CAG TCA GAG CAC GGT CTA ACA GAA GAA ATG ACA ATG AAA
 BamHI A Q S E H G L T E E M T M K

 TAC CGT ATG GAA GGG TGC GTC GAT GGA CAT AAA TTT GTG ATC ACG GGA
 Y R M E G C V D G H K F V I T G

 GAG GGC ATT GGA TAT CCG TTC AAA GGG AAA CAG GCT ATT AAT CTG TGT
 E G I G Y P F K G K Q A I N L C

 GTG GTC GAA GGT GGA CCA TTG CCA TTT GCC GAA GAC ATA TTG TCA GCT
 V V E G G P L P F A E D I L S A

 GCC TTT ATG TAC GGA AAC AGG GTT TTC ACT GAA TAT CCT CAA GAC ATA
 A F M Y G N R V F T E Y P Q D I

 GTT GAC TAT TTC AAG AAC TCG TGT CCT GCT GGA TAT ACA TGG GAC AGG
 V D Y F K N S C P A G Y T W D R

 TCT TTT CTC TTT GAG GAT GGA GCA GTT TGC ATA TGT AAT GCA GAT ATA
 S F L F E D G A V C I C N A D I

 ACA GTG AGT GTT GAA GAA AAC TGC ATG TAT CAT GAG TCC AAA TTC TAT
 T V S V E E N C M Y H E S K F Y

 GGA GTG AAT TTT CCT GCT GAT GGA CCT GTG ATG AAA AAG ATG ACA GAT
 G V N F P A D G P V M K K M T D

 AAC TGG GAG CCA TCC TGC GAG AAG ATC ATA CCA GTA CCT AAG CAG GGG
 N W E P S C E K I I P V P K Q G

 ATA TTG AAA GGG GAT GTC TCC ATG TAC CTC CTT CTG AAG GAT GGT GGG
 I L K G D V S M Y L L L K D G G

 CGT TTA CGG TGC CAA TTC GAC ACA GTT TAC AAA GCA AAG TCT GTG CCA
 R L R C Q F D T V Y K A K S V P

 AGA AAG ATG CCG GAC TGG CAC TTC ATC CAG CAT AAG CTC ACC CGT GAA
 R K M P D W H F I Q H K L T R E

 GAC CGC AGC GAT GCT AAG AAT CAG AAA TGG CAT CTG ACA GAA CAT GCT
 D R S D A K N Q K W H L T E H A

 ATT GCA TCC GGA TCT GCA TTG CCC TGA AAGCTT
 I A S G S A L P * HindIII (SEQ ID NO:29 & 30)

10006922.120401

Figure 12

Amino acid sequence of zFP506 Yellow mutant

MAQSKHGLTKEMTMKYRMEGCVDPGHKQVITGEGIGYPFKGKQAINLCVVEGGPLPFAEDILSAGFKYGDRVFTEYPQDI
VDYFKNSCPAGYTWDRSFLFEDGAVCICNADITVSVEENCMYHESKFYGVNFPADGPVMKKMTDNWEPSCEKIIPVPRQ
GILKGDVSMYLLLLKDGRLRCQFDTVYKAKSVPRKMPDWHFIQHKLTREDRSDAKNQKWHLTEHAIASGSALP*
(SEQ ID NO:31)

Figure 13

Amino Acid Sequence of zFP506 Yellow/bright mutant

MAQSKHGLTKEMTMKYRMEGCVDPGHKQVITGEGIGYPFKGKQAINLCVVEGGPLPFAEDILSAGFKYGDRVFTEYPQDI
VDYFKNSCPAGYTWDRSFLFEDGAVCICNADITVSVEENCMYHESKFYGVNFPADGPVMKKMTDNWEPSCEKIIPVPRQ
GILKGDVSMYLLLLKDGRLRCQFDTVYKAKSVPRKMPDWHFIQHKLTREDRSDAKNQKWHLTEHAIASGSALS*
(SEQ ID NO:32)

1006922-120401



Figure 14

Non-aggregating mutant FP4-NA was generated from zFP538-M128V (humanized version). In comparison with zFP538-M128V, FP4-NA contains two additional amino acid substitutions - K5E and K9T. Also, two accidental nucleotide substitutions were introduced due to PCR mistakes (double underline).

Cloning into pQE30 was done using BamHI and HindIII sites:

```

GGA TCC GCC CAC AGC GAG CAC GGC CTG ACC GAG GAG ATG ACC ATG AAG
BamHI  A  H  S  E  H  G  L  T  E  E  M  T  M  K

TAC CAC ATG GAG GGC TGC GTG AAC GGC CAC AAG TTC GTG ATC ACC GGC
Y  H  M  E  G  C  V  N  G  H  K  F  V  I  T  G

GAG GGC ATC GGC TAC CCC TTC AAG GGC AAG CAG ACC ATC AAC CTG TGC
E  G  I  G  Y  P  F  K  G  K  Q  T  I  N  L  C

GTG ATC GAG GGC GGC CCC CTG CCC TTC AGC GAG GAC ATC CTG AGC GCC
V  I  E  G  G  P  L  P  F  S  E  D  I  L  S  A

GGC TTC AAG TAC GGC GAC CGG ATC TTC ACC GAG TAC CCC CAG GAC ATC
G  F  K  Y  G  D  R  I  F  T  E  Y  P  Q  D  I

GTG GAC TAC TTC AAG AAC AGC TGC CCC GCC GGC TAC ACC TGG GGC CGG
V  D  Y  F  K  N  S  C  P  A  G  Y  T  W  G  R

AGC TTC CTG TTC GAG GAC GGC GCC GTG TGC ATC TGT AAC GTG GAC ATC
S  F  L  F  E  D  G  A  V  C  I  C  N  V  D  I

ACC GTG AGC GTG AAG GAG AAC TGC ATC TAC CAC AAG AGC ATC TTC AAC
T  V  S  V  K  E  N  C  I  Y  H  K  S  I  F  N

GGC GTG AAC TTC CCC GCC GAC GGC CCC GTG ATG AAG AAG ATG ACC ACC
G  V  N  F  P  A  D  G  P  V  M  K  K  M  T  T

AAC TGG GAG GCC AGC TGC GAG AAG ATC ATG CCC GTG CCTA AAG CAG GGC
N  W  E  A  S  C  E  K  I  M  P  V  P  K  Q  G

ATC CTG AAG GGC GAC GTG AGC ATG TAC CTG CTG CTG AAG GAC GGC GGC
I  L  K  G  D  V  S  M  Y  L  L  L  K  D  G  G

CGG TAC CGG TGC CAG TTC GAC ACC GTG TAC AAG GCC AAG AGC GTG CCC
R  Y  R  C  Q  F  D  T  V  Y  K  A  K  S  V  P

AGC AAG ATG CCC GAG TGG CAC TTC ATC CAG CAC AAG CTG CTG CGG GAG
S  K  M  P  E  W  H  F  I  Q  H  K  L  L  R  E

GAC CGG AGC GAC GCC AAG AAC CAG AAG TGG CAG CTG ACC GAG CAC GCC
D  R  S  D  A  K  N  Q  K  W  Q  L  T  E  H  A

ATC GCC TTC CCC AGC GCC CTG GCC TGA AAGCTT
I  A  F  P  S  A  L  A  * HindIII (SEQ ID NOS: 33-34)

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10006922-120401

FIGURE 16

Nucleic acid sequence of humanized drFP583

ATGGTGCGCTCCTCCAAGAACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGG
AGGGCACCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCC
TACGAGGGCCACAACACCGTGAAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTC
GCCTGGGACATCCTGTCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACC
CCGCCGACATCCCCGACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGC
GCGTGATGAACTTCGAGGACGGCGGCGTGGTGACCGTGACCCAAGACTCCTCCCTGC
AGGACGGCTGCTTCATCTACAAGGTGAAGTTCATCGGCGTGAAGTTCCCCTCCGACGG
CCCCGTAATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCC
CCGCGACGGCGTGCTGAAGGGCGAGATCCACAAGGCCCTGAAGCTGAAGGACGGCG
GCCACTACCTGGTGGAGTTCAAGTCCATCTACATGGCCAAGAAGCCCGTGCAGCTGCC
CGGCTACTACTACGTGGACTCCAAGCTGGACATCACCTCCCACAACGAGGACTACAC
CATCGTGGAGCAGTACGAGCGCACCGAGGGCCGCCACCACCTGTTCTGTAG (SEQ ID
NO:35)

Figure 17

DNA sequence (ORF) of E5-NA

ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGCACCGTGAACGGCCACGAGT
TCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCCTACGAGGGCCACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCCC
CCTGCCCTTCGCTGGGACATCCTGTCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATC
CCCCGACTACAAGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGGCGA
CCGTGACCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTACAAGGTGAAGTTCATCGGCGTGAAGTTCCCCTCCGA
CGGCCCCGTGATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCGCGACGGCGTGCTGAAG
GGCGAGATCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATCTACATGGCCAAGA
AGCCCGTGCAGTGCCCGGCTACTACTACGTGGACACCAAGCTGGACATCACCTCCCACAACGAGGACTACACCATCGT
GGAGCAGTACGAGCGCACCGAGGGCCGCCACCACCTGTTCTGTAA (SEQ ID NO:36)

Figure 18

ATGGTGCGCT CCTCCAAGAA CGTCATCAAG GAGTTCATGC GCTTCAAGGT
GCGCATGGAGGGCACCGTGA ACGGCCACGA GTTCGAGATC GAGGGCGAGG GCGAGGGCCG
CCCCTACGAG GGCCACAACA CCGTGAAGCT GAAGGTGACC AAGGGCGGCC CCCTGCCCTT
CGCTGGGAC ATCCTGTCCC CCCAGTTCCA GTACGGCTCC AAGGTGTACG TGAAGCACCC
CGCCGACATC CCGGACTACA AGAAGCTGTC CTTCCCCGAG GGCTTCAAGT GGGAGCGCGT
GATGAACTTCGAGGACGGCG GCGTGGCGAC CGTGACCCAA GACTCCTCCC TGCAGGACGG
CTGCTTCATC TACAAGGTGA AGTTCATCGG CGTGAAGTTC CCCTCCGACG GCCCCGTAAT
GCAGAAGAAG ACCATGGGCT GGGAGGCCTC CACCGAGCGC CTGTACCCCC GCGACGGCGT
GCTGAAGGGC GAGACCCACA AGGCCCTGAA GCTGAAGGAC GGCGGCCACT ACCTGGTGGA
GTTCAAGTCC ATCTACATGG CCAAGAAGCC CGTGCAGCTG CCCGGCTACT ACTACGTGGA
CGCCAAGCTG GACATCACCT CCCACAACGA GGAATACACC ATCGTGGAGC AGTACGAGCG
CACCGAGGGCCGCCACCACC TGTTCTGTGA G (SEQ ID NO:37)

1006922-120401

Figure 19.

Nucleic acid sequence FP6 (E57)-NA

ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGCACCGTGA
ACGGCCACGAGTTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCTACGAGGGCCACAACACCGTG
AAGCTGAAGGTGACCAAGGGCGGCCCTGCCCTTCGCCTGGGACATCCTGTCCCCCAGTTCCAGT
ACGGCTCCAAGGTGTACGTGAAGCACCCGCGGACATCCCCGACTACAAGAAGCTGTCCTTCCCCGA
GGGCTTCAAGTGGGAGCGCGTGATGAACCTCGAGGACGGCGGCGTGGCGACCGTGACCCAGGACTC
CTCCCTGCAGGACGGCTGCTTCATCTACAAGGTGAAGTTCATCGGCGTGAACCTCCCTCCGACGGC
CCCGTGATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCGCGACGGC
GTGCTGAAGGGCGAGACCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTC
AAGTCCATCTACATGGCCAAGAAGCCCGTGACGCTGCCCGGCTACTACTACGTGGACGCCAAGCTGG
ACATCACCTCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCACCGAGGGCCGCCACCA
CCTGTTCTG (SEQ ID NO:38)

1006923.120401

Figure 20.

Non-aggregating mutant FP7-NA was generated from M35-5 (FP7a). In comparison with M35-5, FP7-NA contains two additional substitutions - K6T and K7E. Nucleotide substitutions in the codon for Leu-4 were introduced to optimize codon usage (double underline).

Cloning into pQE30 was done using BamHI and HindIII sites:

```

GGA TCC GCC TCC CTG CTG ACC GAG ACC ATG CCC TTC AGG ACC ACC ATC
BamHI  A  S  L  L  T  E  T  M  P  F  R  T  T  I

GAG GGC ACC GTG AAC GGC CAC TAC TTC AAG TGC ACC GGC AAG GGC GAG
E  G  T  V  N  G  H  Y  F  K  C  T  G  K  G  E

GGC AAC CCC CTC GAG GGC ACC CAG GAG ATG AAG ATC GAG GTG ATC GAG
G  N  P  L  E  G  T  Q  E  M  K  I  E  V  I  E

GGC GGC CCC CTG CCC TTC GCC TTC CAC ATC CTG TCC ACC TCC TGC ATG
G  G  P  L  P  F  A  F  H  I  L  S  T  S  C  M

TAC GGC TCC AAG GCC TTC ATC AAG TAC GTG TCC GGC ATC CCC GAC TAC
Y  G  S  K  A  F  I  K  Y  V  S  G  I  P  D  Y

TTC AAG CAG TCC CTC CCC GAG GGC TTC ACC TGG GAG CGC ACC ACC ACC
F  K  Q  S  L  P  E  G  F  T  W  E  R  T  T  T

TAC GAG GAC GGC GGC TTC CTG ACC GCC CAC CAG GAC ACC TCC CTG GAC
Y  E  D  G  G  F  L  T  A  H  Q  D  T  S  L  D

GGC GAC TGC CTG GTG TAC AAG GTG AAG ATC CTG GGC AAC AAC TTC CCC
G  D  C  L  V  Y  K  V  K  I  L  G  N  N  F  P

GCC GAC GGC CCC GTG ATG CAG AAC AAG GCC GGC CGC TGG GAG CCC TCC
A  D  G  P  V  M  Q  N  K  A  G  R  W  E  P  S

ACC GAG ATC GTG TAC GAG GTG GAC GGC GTG CTG CGC GGC CAG TCC CTG
T  E  I  V  Y  E  V  D  G  V  L  R  G  Q  S  L

ATG GCC CTG GAG TGC CCC GGC GGT CGC CAC CTG ACC TGC CAC CTG CAC
M  A  L  E  C  P  G  G  R  H  L  T  C  H  L  H

ACC ACC TAC CGC TCC AAG AAG CCC GCC TCC GCC CTG AAG ATG CCC GGC
T  T  Y  R  S  K  K  P  A  S  A  L  K  M  P  G

TTC CAC TTC GAG GAC CAC CGC ATC GAG ATC CTG GAG GAG GTG GAG AAG
F  H  F  E  D  H  R  I  E  I  L  E  E  V  E  K

GGC AAG TGC TAC AAG CAG TAC GAG GCC GCC GTG GGC CGC TAC TGC GAC
G  K  C  Y  K  Q  Y  E  A  A  V  G  R  Y  C  D

GCC GCC CCC TCC AAG CTG GGC CAC AAC TGAAGCTT
A  A  P  S  K  L  G  H  N  * HindIII (SEQ ID NO:39 & 40)

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104021-2269001

FIGURE 21

ATG GCC TCC **TTC** CTG AAG AAG **ACC** ATG CCC TTC **AAG** ACC ACC ATC GAG
 M A S F L K K T M P F K T T I E

 GGC ACC GTG AAC GGC CAC TAC TTC AAG TGC ACC GGC AAG GGC GAG GGC
 G T V N G H Y F K C T G K G E G

 AAC CCC **TTC** GAG GGC ACC CAG GAG ATG **AAG** ATC GAG GTG ATC GAG GGC
 N P F E G T Q E M K I E V I E G

 GGC CCC CTG CCC TTC GCC TTC CAC ATC CTG TCC ACC TCC TGC ATG TAC
 G P L P F A F H I L S T S C M Y

 GGC TCC AAG GCC TTC ATC AAG TAC **GTG** TCC GGC ATC CCC GAC TAC TTC
 G S K A F I K Y V S G I P D Y F

 AAG CAG TCC **TTC** CCC GAG GGC TTC ACC TGG GAG CGC ACC ACC ACC TAC
 K Q S F P E G F T W E R T T T Y

 GAG GAC GGC GGC **TTC** CTG ACC GCC CAC CAG GAC ACC TCC CTG GAC GGC
 E D G G F L T A H Q D T S L D G

 GAC TGC CTG GTG TAC AAG GTG AAG ATC CTG GGC AAC AAC TTC CCC GCC
 D C L V Y K V K I L G N N F P A

 GAC GGC CCC GTG ATG CAG AAC AAG GCC GGC CGC TGG GAG CCC TCC ACC
 D G P V M Q N K A G R W E P S T

 GAG ATC GTG TAC GAG GTG GAC GGC GTG CTG CGC GGC CAG TCC CTG ATG
 E I V Y E V D G V L R G Q S L M

 GCC CTG **AAG** TGC CCC GGC GGC CGC CAC CTG ACC TGC CAC CTG CAC ACC
 A L K C P G G R H L T C H L H T

 ACC TAC CGC TCC AAG AAG CCC GCC TCC GCC CTG AAG ATG CCC GGC TTC
 T Y R S K K P A S A L K M P G F

 CAC TTC GAG GAC CAC CGC ATC GAG **ATC** **ATG** GAG GAG GTG GAG AAG GGC
 H F E D H R I E I M E E V E K G

 AAG TGC TAC AAG CAG TAC GAG GCC GCC GTG GGC CGC TAC TGC **GAC** GCC
 K C Y K Q Y E A A V G R Y C D A

 GCC CCC TCC AAG CTG GGC CAC AAC TgA
 A P S K L G H N * (SEQ ID NO:41 & 42)

10006922-12040-1
 10006922-12040-1

Figure 22

Sequence of humanized 6/9 hybrid gene and 6/9-Q3 mutant

Sequence of nucleotide 3' by 3' for 6/9-2G and 6/9-Q3																		CAG(Q)	
1	ATG	AGC	TGC	AGC	AAG	AAC	GTG	ATC	AAG	GAG	TTC	ATG	CGG	TTC	AAG	GTG		48	
1	M	S	C	S	K	N	V	I	K	E	F	M	R	F	<u>K</u>	V		16	
49	CGG	ATG	GAG	GGC	ACC	GTG	AAC	GGC	CAC	GAG	TTC	GAG	ATC	AAG	GGC	GAG		96	
17	R	M	E	G	T	V	N	G	H	E	F	E	I	K	G	E		32	
97	GGC	GAG	GGC	CGG	CCC	TAC	GAG	GGC	CAC	TGC	AGC	GTG	AAG	CTC	ATG	GTG		144	
33	G	E	G	R	P	Y	E	G	H	C	S	V	K	L	M	V		48	
145	ACC	AAG	GGC	GGC	CCC	CTC	CCC	TTC	GCC	TTC	GAC	ATC	CTC	AGC	CCC	CAG		192	
49	T	K	G	G	P	L	P	F	A	F	D	I	L	S	P	Q		64	
193	TTC	CAG	TAC	GGC	AGC	AAG	GTG	TAC	GTG	AAG	CAC	CCC	GCC	GAC	ATC	CCC		240	
65	F	Q	Y	G	S	K	V	Y	V	K	H	P	A	D	I	P		80	
ATG(M) for 6/9-Q3																			
241	GAC	TAC	AAG	AAG	CTC	AGC	TTC	CCC	GAG	GGC	TTC	AAG	TGG	GAG	CGG	GTG		288	
81	D	Y	<u>K</u>	K	L	S	F	P	E	G	F	K	W	E	R	V		96	
289	ATG	AAC	TTC	GAG	GAC	GGC	GGC	GTG	GTG	ACC	GTG	AGC	CAG	GAC	AGC	AGC		336	
97	M	N	F	E	D	G	G	V	V	T	V	S	Q	D	S	S		112	
337	CTC	AAG	GAC	GGC	TGC	TTC	ATC	TAC	GAG	GTG	AAG	TTC	ATC	GGC	GTG	AAC		384	
113	L	K	D	G	C	F	I	Y	E	V	K	F	I	G	V	N		128	
385	TTC	CCC	AGC	GAC	GGC	CCC	GTG	ATG	CAG	CGG	CGG	ACC	CGG	GGC	TGG	GAG		432	
129	F	P	S	D	G	P	V	M	Q	R	R	T	R	G	W	E		144	
433	GCC	AGC	AGC	GAG	CGG	CTC	TAC	CCC	CGG	GAC	GGC	GTG	CTC	AAG	GGC	GAC		480	
145	A	S	S	E	R	L	Y	P	R	D	G	V	L	K	G	D		160	
481	ATC	CAC	ATG	GCC	CTC	CGG	CTC	GAG	GGC	GGC	GGC	CAC	TAC	CTC	GTG	GAG		528	
161	I	H	M	A	L	R	L	E	G	G	G	H	Y	L	V	E		176	
529	TTC	AAG	AGC	ATC	TAC	ATG	GCC	AAG	AAG	CCC	GTG	CAG	CTC	CCC	GGC	TAC		576	
177	F	K	S	I	Y	M	A	K	K	P	V	Q	L	P	G	Y		192	
577	TAC	TAC	GTG	GAC	AGC	AAG	CTC	GAC	ATC	ACC	AGC	CAC	AAC	GAG	GAC	TAC		624	
193	Y	Y	V	D	S	K	L	D	I	T	S	H	N	E	D	Y		208	
TCC(S) for 6/9-2G and 6/9-Q3																			
625	ACC	ATC	GTG	GAG	CAG	TAC	GAG	CGG	ACC	GAG	GGC	CGG	CAC	CAC	CTC	TTC		672	
209	T	I	V	E	Q	Y	E	R	<u>T</u>	E	G	R	H	H	L	F		224	
673	CTC	TGA																678	
225	L	*																226	

(SEQ ID NO:43 & 44)

T04027 "22690001